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Twenty-Five Thousand-Year-Old Triple Burial From Dolní Věstonice: An Ice-Age Family?

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ABSTRACT In 1986 a palaeolithic triple burial was discovered near Dolní Věstonice (Czech Republic). The occurrence of anatomic variants in all three skeletons gave rise to speculations that the buried individuals may have been closely related. To test this hypothesis the skeletons were submitted to a systematic kinship analysis based on odontologic and other non-metric traits. Statistical tests showed that the coincident occurrence of several rare traits in the individuals is highly unlikely to occur at random. This and further data included in the analysis therefore suggest that the three individuals buried together were genetically related and actually belonged to one family. Am J Phys Anthropol 102:123–131. © 1997 Wiley-Liss, Inc.

Dolní Věstonice in Moravia is among the most important upper palaeolithic sites in Central Europe. Since the onset of systematic excavations in 1924, rich inventories of stone and bone tools as well as exceptional works of art have been unearthed time and again. Among the most spectacular finds are the "Venus of Dolní Věstonice," a female figurine of baked clay, and a woman's head carved from mammoth ivory representing one of the few realistic portraits known from palaeolithic times (Absolon, 1938; Klíma, 1963, 1983; Vandiver et al., 1989). In addition, Dolní Věstonice has yielded a large number of human skeletal remains. Up to the present, the remains of at least 35 individuals have been discovered, six of whom were encountered in proper graves. Each burial seems to have been accompanied with extensive ritual (Klíma, 1990).

In 1986, during an excavation by the Archaeological Institute of the Czechoslovakian Academy of Sciences, an exceptionally well-preserved triple burial was discovered in a cultural layer 5 m below the surface (Klíma, 1988; Jelínek, 1992). Three young individuals, two men and one woman, lay extended side by side, their bodies strewn with red ochre (Fig. 1). From the excavator's perspective, the male on the right (DV 14) was determined to be 16–17 years of age, the male on the left (DV 13) to be 17–18. Between them lay a female (DV 15) of about 20. Charcoal from the occupational layer was radiocarbon-dated 27,660 ± 80 BP (GrN-

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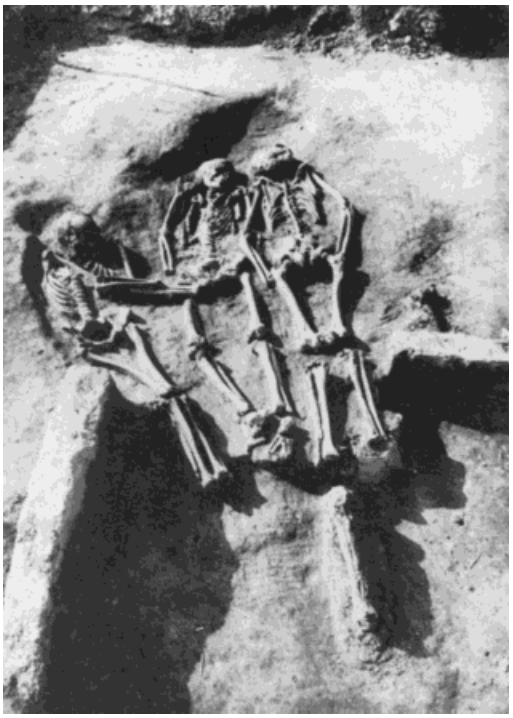

Fig. 1. The upper palaeolithic triple burial discovered in the Pavlov hills above the village of Dolní Věstonice, Moravia, Czech Republic. The bodies were partially covered with red ochre; grave goods included silex knives, ornamental shells of Tertiary snails, and pierced animal teeth (*Alopex lagopus*, *Canis lupus*) as well as pendants of mammoth ivory formerly attached to headbands. Individuals from left to right: DV 13, DV 15, DV 14 (photo: S. Skoupý).

13692) and 26,640 ± 110 BP (GrN-14831; Vlček, 1991, 1992). Culturally the finds can be assigned to the Pavlovian, a local variant of the Eastern Gravettian technocomplex (Klíma, 1983; Pichler, 1996).

A routine anthropological analysis of the skeletons revealed that all three individuals shared characteristic shapes of the scapula and aplasia of the right frontal sinus. The agreement in these rare anatomic variants seemed to suggest that the individuals were related, and may even have been siblings (Vlček, 1995). A systematic kinship analysis based on a recently developed set of odontologic and other non-metric traits (Alt and Vach, 1994; Alt, 1997; Alt et al., in preparation) was conducted to test this hypothesis.

MATERIALS AND METHODS

Morphologic traits

Traits used in kinship analysis must be selected for their high heritability, low frequency, distinct expression, low dependence on age and sex, and small intertrait correlation (Saunders, 1989). In the past, various trait classes have been used in attempts to establish kinship in skeletal remains. Studies were based on osteometrical criteria, on serological features, radiograms of the skull, and, most frequently, on epigentic traits (Berry and Berry, 1967; Corruccini, 1974; Sjøvold, 1984; Hauser and De Stefano, 1989; Saunders, 1989). With all of these trait classes, major problems arose from a lack of information on the heritability of the traits, and from the difficulties of obtaining such information. In view of the requirements stated above, odontologic traits are especially well-suited for the determination of genetic relationships in skeletal remains. They are simple to identify, are easily validated in clinical studies, and information on the heredity of many traits is already available (Alt, 1997; see also Dahlberg, 1971; Scott, 1973; Sharma and Corruccini, 1986; Schulze, 1987; Nichol, 1990). In the analysis of prehistoric skeletal material, the (generally) better state of preservation of teeth and jaws in comparison to other skeletal parts represents a further advantage of odontological traits.

The catalogue of traits developed for odontologic kinship analysis consists of 137 basic traits. These include variants of tooth crowns and roots, ontogenetic disturbances of the shape, number, size, structure, and position of teeth, and selected non-metric traits of the cranium and jaws (Alt, 1997). Table 1 provides some examples of basic traits organized according to tooth groups. Some of the traits follow the Mendelian laws, but the majority of traits are controlled polygenously, i.e., the quasi-continuous variation of their expression is influenced both genetically and environmentally (additive genes effect). Each trait can usually occur on several teeth, some traits can be expressed in a number of different vari-

TABLE 1. Selected examples of the 137 basic traits used in odontologic kinship analysis

Trait	Expression[1]
Variants of mandibular molar crowns and roots	
Number of main cusps[2]	3; 4; 5; 6
Cusp reduction	Absent; hypoconulid. Entoconid, hypoconid. Combined forms
Fissure pattern[2]	Y-shaped; +-shaped: X-shaped
Number of roots[2]	1; 2; 3
Additional root by differentiation	Absent; mesial, distal
Types of root fusion	Absent; buccal, medial, Lingual, combined forms
Anomalies of mandibular molar crowns	
Paracone tubercle	Absent; present
Tuberculum intermedium (C-7)	Absent; present
Paramolar tubercle (Ridge, groove, small pit, slight/moderate/large tubercle)[2]	Absent; present
Citroën tubercle (ridge, groove, small pit, slight/moderate/large tubercle)	Absent; present
Entoconulid (C-6)[2]	Absent; present
Deflecting wrinkle	Absent; present
Foramina moralia[2]	Absent; present
Overdeveloped cusps (protoconid, metaconid)	Absent; present
Anomalies of maxillary molar crowns	
Carabelli tubercle (ridge, groove, small pit, slight/moderate/large tubercle)	Absent; present
Paramolar tubercle (ridge, groove, small pit, slight/moderate/large tubercle)	Absent; present
Over-developed cusps (hypocone; protocone; paracone; combined forms)[2]	Absent; present
Accessory cusplets in the mesial marginal ridge area (MAT; PL; MPT; combinations)	Absent; present
Accessory cusplet central of the mesial marginal ridge (LPT)	Absent; present
Accessory cusplet in the distal marginal ridge area (DAT)[2]	Absent; present
Accessory cusplet central of the distal marginal ridge (ML)[2]	Absent; present
Compressed crown	Absent; present

[1]Expression = possible variants of trait expression.
[2]Traits present in at least two individuals from the Dolní Věstonice triple burial (see also Table 3).

ants (cf. Table 1). As a result, there are more than 1,000 individual traits or variants of traits potentially observable in each individual. Additionally, each new analysis may also include specific traits beyond the established catalogue if there is a conspicuous occurrence of rare (skeletal) variants or hereditary anomalies in the investigated group.

The usefulness of this set of traits for kinship analysis has been established in a number of previous applications, e.g., in a test of "genetic" kinship on two adults and six children from a Bronze Age storage pit (Alt et al., 1995c), in the identification of "family" members and unrelated servants among murdered inhabitants of a Late-Roman villa rustica (Alt et al., 1995b), in kinship analyses of Early Medieval cemeteries with several hundred graves (Alt et al., in preparation), and on other skeletal material (Alt and Vach, 1995; Alt et al., 1995a).

In the Dolní Věstonice triple burial, aplasia of the right frontal sinus and characteristic shapes of the scapula shared by all three individuals gave rise to speculations that the buried individuals may have been closely related (Vlček, 1991). An odontologic kinship analysis was conducted either to corroborate or to refute this bold postulation. The exceptional state of preservation of the ice-age skeletons enabled us to evaluate over 900 of the nearly 1,100 characteristics potentially observable in each of the three individuals. This represents an excellent data base for our attempt.

Each trait can either be present, absent, or indiscernible (if the specific skeletal part is missing or insufficiently preserved). In the present analysis, we concentrate on those characteristics present in at least two of the three individuals. These include 23 morphological variants of dental crowns and roots,

12 dental anomalies, and 6 epigenetic variants of skull and jaws. Three of these traits (aplasia of the frontal sinus, torus acusticus, impaction of third molars) were selected as being of special value for establishing "genetic" relations among group members, because all of these traits are present in each of the individuals, all are rare in the population in general (≤5%), and there is established information on the genetic determination and on increased familial occurrences of the specific characteristics (cf. Szilvassy, 1982; Tal and Tau, 1984; Schulze, 1987; Hauser and De Stefano, 1989; Alt, 1997).

Statistical approaches

The basic idea in kinship analysis is to infer biological relationships from the increased occurrence of rare, genetically determined traits. In analysing the data matrix containing the registered traits, the decisive step is to identify clues at genetically linked group members (cf. Alt and Vach, 1994). The type of burial, respectively its archaeological or forensic classification (multiple burial, mass or collective grave, cemetery etc.), is a determining factor in selecting an appropriate approach for the identification of the looked-for structures in the data. For each approach, specific algorithms had to be developed to identify "suspicious" (possibly related) individuals. Basically, the analysis has to be narrowed to groups of individuals showing a number of corresponding traits. The state of preservation of the skeletal material represents a limiting factor in the analysis, as the detection of kinship is possible only if a sufficiently large number of traits can be evaluated.

In multiple or collective burials, the question of potential genetic relationships among individuals arises quite naturally, especially if the individuals were buried simultaneously, as in the present case. Indications of genetic relationships in a small group of simultaneously buried individuals result from the increased occurrence of traits which are rare in the population in general (or any randomly selected group from this population). The increased occurrence of these traits among the investigated individuals can then be explained by inheritance, which defines the traits as being "typical" for the detected family. So for each family (group of genetically related individuals) there is, in principle, a set of (hereditary) traits typical of this family (Sjøvold, 1975; Stewart and Prescott, 1976; Lee and Goose, 1982; Schulze, 1987). Hence, if the three individuals from Dolní Věstonice are genetically related, there should be striking agreement in such a set of traits among them.

The decisive step in the data analysis is to identify those traits in the data matrix which are most valuable for detecting possible kinship relations in the specific group of individuals. Initially, intragroup frequencies for all registered traits are calculated and compared to the frequencies of the respective traits in a corresponding reference population. On the basis of their increased frequencies in the considered group, a number of traits are then selected for further analysis. The question that arises at this point is whether the increased frequencies of the traits can be explained by random coincidences or whether they are statistically significant.

This problem is approached by defining an appropriate null hypothesis which is to be rejected by standardized statistical tests. The null hypothesis states that the investigated individuals were randomly chosen from the reference population. As a result, traits should occur both independently among the investigated individuals and they should occur with a probability equal to the relative frequency of the specific trait in the reference population. Using the binomial law, we can compute the p value for each trait, i.e., we compute the probability of observing at least the actually observed number of individuals exhibiting the trait under the null hypothesis. The computation of the p value for a specific trait which is observable in K individuals, present in k individuals, and which occurs with a relative frequency q in the reference population is based on the formula

$$\sum_{j=k}^{K} \binom{K}{k} \mathrm{q}^k \, (1 - \mathrm{q})^{K-k}$$

Small p values indicate that the frequencies of the considered traits are indeed increased in the investigated group. Yet with

regard to the number of traits examined, the occurrence of some small *p* values is not sufficient for the rejection of the null hypothesis. In order to achieve this, a multiple statistical test procedure, e.g., the Bonferroni procedure, has to be applied to the data. The Bonferroni procedure enables us to compute a global *p* value by multiplying the minimal *p* value by the number n of tests performed. In this specific case, n is chosen equal to the number of traits observable in at least two individuals, as only those can contribute to the analysis. If the computed global *p* value is smaller than a pre-defined level α, the null hypothesis can be rejected.

Rejection of the null hypothesis implies that the coincident occurrence of specific traits in the investigated group arises from a systematic source—the existence of genetic relations among the individuals. The level α value controls the probability of an type-I-error, i.e., the probability of postulating genetic relations based on the rejection of the null hypothesis even though the null hypothesis is true.

A further aspect to be considered in the validation of the results concerns the value of the individual traits for establishing kinship. The highest value is assigned to traits which are rare in the population in general and for which there is well-founded knowledge on the heritability of the specific trait. High-value traits with small *p* values are more significant than low-value traits with small *p* values. The similarity or dissimilarity of the individuals in pairs with regard to specific sets of traits as well as the amount of missing values are further factors which influence the validity of the results and have to be considered in the statistical analysis of the data (for a detailed discussion of evaluation and validation procedures see Alt and Vach, 1992, 1994, 1995; Vach and Alt, 1993).

RESULTS AND DISCUSSION

Our investigation revealed a number of traits occurring in two or three individuals from the triple burial. The fact that the three individuals agree in a certain number of traits is a first indication of possible "genetic" relationships among them. Since the more uncommon a trait is in a given population the more valuable it is for establishing kinship, we selected three rare traits present in each of the three individuals for a conclusive statistical test. The selected traits include unilateral absence of the frontal sinus, the occurrence of specific auditory exostoses, and impaction of the upper wisdom teeth.

Aplasia of the right frontal sinus in all of the individuals is among the traits which gave rise to speculations on possible "familial" relationships in the course of the original anthropological analysis (Vlček, 1995). It represents an example of a trait which is not part of the regular list of traits, but is included in the analysis for its conspicuous occurrence in this specific group. A strong genetic determination of size and shape of the frontal sinus was established on large family samples (Szilvassy, 1982). Frequencies for the absence of the frontal sinus were determined to be 4 to 8% for bilateral aplasia, 3 to 5% for aplasia of the right, and 2 to 3% for aplasia of the left sinus (Wagemann, 1964; Szilvassy, 1982; Hauser and De Stefano, 1989). Our statistical analysis is based on an average frequency for aplasia of the right frontal sinus of 4%.

The presence of specific auditory exostoses (torus acusticus) represents another trait common to all three individuals. In the literature, both irritation (e.g., through frequent exposure to cold water) and genetic factors are discussed as causes. Exostoses in the region of the auditory opening have to be distinguished in two basic variants: an external and an internal type. According to Mann (1984), only the internal type is caused by irritations, whereas genetic predisposition controls the occurrence of the external torus acusticus. Genetic determination of the trait is supported by increased familial occurrences (Hauser and De Stefano, 1989). Prevalences range from 0% to 14.3%, with the highest frequencies always being found among American Indians (Kessel, 1924; Cosseddu et al., 1979; Perizonius, 1979; Sjøvold, 1984; Hauser and De Stefano, 1989). In prehistoric and modern European skeletal samples, frequencies for external auditory exostoses are generally well below the 5% we used in our statistical calculations.

The third trait we selected is impaction of upper third molars. Whereas the impaction

TABLE 2. Three rare traits occurring in all individuals from the Doliní Věstonice palaeolithic triple burial

	DV 13	DV14	DV15	cf (%)[1]	*p* value[2]
Unilateral aplasia of frontal sinus	−+	−+	−+	4.0	0.000064
Torus acusticus	++	?+	++	5.0	0.000125
Impaction of upper third molars	+−	++	++	1.0	0.000001

[1]cf: Relative frequency of trait observed in reference populations.
[2]*p* value: Probability of random agreement of the individuals under the assumption that a trait occurs with the probability cf.
+, trait present; −, trait absent; ?, trait indiscernible because of missing or insufficiently preserved skeletal part.

of wisdom teeth is regularly found to be around 20% in extant populations (or even higher in specific groups), it is much less developed in earlier populations and rarely occurs in palaeolithic material (Klatsky, 1956; Dachi and Howell, 1961; Brabant and Twisselmann, 1964; Wei, 1988). This diachronic increase in frequency is attributed to an evolutionary trend towards a size reduction of the masticatory apparatus. In the course of this development, the decrease of jaw size progresses more rapidly than the reduction of tooth size, the resulting insufficiency in jaw length favouring impaction (Schilli and Krekeler, 1984; Henke and Rothe, 1994; Wei, 1996). Soft diets, respectively the reduction of masticatory stress by advanced techniques in food preparation, appear to have accelerated this process notably since neolithic times (Brace, 1995; Wei 1996). Average frequencies for impaction have been reported to be 4.4% for the Middle Ages, 2.8% for Roman times, 1.6% for the Neolithic, and below 1% for the Palaeolithic (Brabant and Twisselmann, 1964; Schilli and Krekeler 1984; Alt, 1997). In view of the near 0% frequencies given for several palaeolithic and mesolithic samples, our calculations are based on a frequency of impaction of the upper wisdom teeth of 1%.

By submitting these characteristics to a number of test procedures, we tried to establish whether or not the common occurrence of three rare traits in all of the individuals from the triple burial is statistically significant. Proceeding under the assumption that all individuals exhibit a specific trait randomly and independently, we first computed the probability of finding at least the actually observed number of individuals showing each trait (trait-specific *p* values). In this computation the probability that a specific trait is present in any individual is chosen equal to the frequency of that trait in the reference population (for discussion on the selection of appropriate reference populations, see Alt and Vach, 1994, 1995; Alt et al., 1995c).

In the present case, the probability of random agreement is small for each of the selected traits (Table 2). The calculated *p* values thus suggest that we may indeed have detected a group of traits "typical" of the Dolní Věstonice "family." However, as the analysis included 1,088 traits per individual, 739 of which could be evaluated at least twice, the occurrence of some small *p* values might represent a random effect. The Bonferroni procedure makes it possible to combine the trait-specific *p* values to arrive at an overall measure for the statistical significance of our findings. The global *p* value of 0.0007 obtained from this procedure permits us to reject the null hypothesis stating that the three individuals independently exhibit the traits with a probability equal to their relative frequencies in a reference population.

We thereby obtained statistical evidence that the coincident expression of these three rare traits in each individual from Dolní Věstonice is extremely unlikely to occur at random, suggesting that the hypothesis that the three individuals belong to the same "family" is true. Yet this conclusion could still be said to rely on a very small number of traits. Table 3 shows that the actual number of traits co-occurring in two or three of the individuals is considerably larger than the three traits selected for demonstrative purposes. Even more suggestive of a close relationship is the fact that the number of traits present in all three individuals exceeds the number of traits present in two individuals only—note that in most cases where coincidence is lacking the respective traits were indiscernible because of poor preservation of the skeletal region, possibly masking an

TABLE 3. Traits present in at least two individuals from the Dolní Věstonice triple burial

No.	Trait	DV 13	DV 14	DV 15	nio	nip	cf (%)	Ref.
5	Lingual surface 13 23 (var 1)	??	++	++	2	2	—	—
11	Lingual surface 43 33 (var 1)	++	++	++	3	3	—	—
13	Lingual surface 11 21 12 22 (var 1)	????	++++	−−++	2	2	—	—
15	Lingual surface 41 31 42 32 (var 1)	++++	++++	+?+?	3	3	—	—
29	Marginal ridges/distal 43 33	++	++	++	3	3	—	—
49	Tuberculum dentis 11 21 (var 1 2)	??	++	++	2	2	58,0	e
53	Tuberculum dentis 13 23 (var 1)	??	++	++	2	2	75,0	e
94	Fissure pattern 14 24 (var 1)	?+	++	+−	3	3	—	—
100	Fissure pattern 15 25 (var 1)	+?	++	−−	3	2	—	—
109	Fissure pattern 44 34 (var 4)	++	++	++	3	3	—	—
112	Fissure pattern 45 35 (var 1)	++	+−	+?	3	3	—	—
149	Number of roots 44 34 (1)	++	+?	++	3	3	—	—
153	Number of roots 45 35 (1)	++	+?	++	3	3	—	—
169	Cusp reduction 18 28	−+	++	++	3	3	—	—
211	Number of cusps 46 36 (5)	++	++	?+	3	3	—	—
214	Number of cusps 47 37 (4)	++	++	++	3	3	—	—
219	Number of cusps 48 38 (5)	++	??	++	2	2	—	—
248	Fissure pattern 46 36 (var 1)	??	+?	??	2	2	73,0	f
252	Fissure pattern 47 37 (var 1)	+?	−−	++	3	2	29,0	f
258	Fissure pattern 48 38 (var 3)	??	−+	+?	2	2	—	—
261	Number of roots 46 36 (2)	++	++	++	3	3	—	—
266	Number of roots 47 37 (2)	++	++	++	3	3	—	—
271	Number of roots 48 38 (2)	++	++	++	3	3	—	—
433	Overdeveloped cusp 16 26	++	++	??	2	2	—	—
510	Accessory cusp 17 27 (DAT)	−−	++	++	3	2	31,0	a
511	Accessory cusp 18 28 (DAT)	−+	++	++	3	3	42,0	a
514	Accessory cusp 18 28 (ML)	++	−−	++	3	2	18,0	a
525	Entoconulid 48 38	++	??	+?	2	2	4,3	b
527	Foramina molaria 47 37	++	−−	++	3	2	20,0	a
528	Foramina molaria 48 38	++	??	+?	2	2	20,0	a
558	Tuberculum paramolare 48 38	++	??	++	2	2	30,0	a
772	Retention/impaction 18 28	+−	++	++	3	3	1,0	a
796	Retention/impaction 48 38	−−			3	2	1,0	a
820	Anterior crowding/maxilla	−	+	+	3	2	3,8	a
821	Anterior crowding/mandible	+	+	−	3	2	30,0	a
1030	Molar foramen	−−	++	++	3	2	—	—
1072	Tuberculum pharyngeum	+	+	?	2	2	80,0	d
1078	Torus acusticus	++	?+	++	3	3	5,0	d
1083	Foramina zygomatico-facialia	−+	??	+−	2	2	14.6	a
1084	Foram. zygomatico-facial. mult.	+−	??	+−	2	2	57,0	d
1086	Sinus frontalis/aplasia dex.	+−	??	+−	2	2		a
	number of traits observable	35	35	39				
	number of traits present	31	32	37				

nio = number of individuals with trait observable; nip = number of individuals with trait present; cf = relative frequency of trait in reference population; + = trait present; − = trait absent; ? = trait indiscernible because of missing or poorly preserved skeletal part. Numbers following trait designations refer to two-digit tooth numbers according to FI regulations, i.e., the consecutive numbering of teeth by quadrants starting with the upper right first incisor (tooth 11 = 1st tooth in 1st quadrant) and ending with the lower right third molar (tooth 48 = 8th tooth in 4th quadrant; see Türp and Alt, 1995). Ref = reference for comparative frequencies: a, Alt et al., (in prep.); b, Saunders and Mayhall (1982); c, Wagemann (1964); d, Czarnetski (1972); e, Rudo (1969); f, Hellman (1928).

even larger number of traits common to all three individuals. To be specific: of the 41 traits present in at least two of the individuals, 44% are present in all three individuals, i.e. the Dolní Věstonice group shows a frequency of 100% for 18 of the 41 traits. For a further 34% of the traits, complete correspondence is possible but could not be established because of insufficient preservation of the respective skeletal parts. In just 22% of cases did "only" two individuals correspond. Furthermore, differentiation of individuals within the group does not seem possible on the basis of the selected traits, as each individual shows approximately the same number of expressed traits (Table 3). Neither are there increased similarities in pairs.

These findings are exactly what one expects in a family, which is a group of closely related individuals. Siblings share 50% of their genes. As hereditary traits are passed from parents to children, the probability of finding rare traits is increased if one searches within the family. A hypothetical "family" should therefore correspond in a large number of phenotypical traits.

Prehistoric kinship analysis represents an attempt to establish the similarity or dissimilarity of individuals on the basis of external skeletal variants. The exact processes of transmission for morphognostic traits are more or less unknown, although there is agreement on the facts that genetic factors play a role in their development and that environmental factors modify their expression. Morphognostic characteristics can therefore be used for establishing phenotypical similarities among individuals but not for genetic analyses at the genotypic level. In the case of the triple burial from Dolní Věstonice, a number of clues detected in the data, especially the extent of the correspondences between the individuals and the statistical significance of the "family's" (typical) set of traits, enable us to deduce genetic relations from phenotypical agreement. This inference by polysymptomatic estimation of similarity is a well-established procedure, e.g., in morphological paternity testing (Knuβmann, 1988). Generally such an analysis does not permit any conclusions regarding the degree of relationship among individuals. However, as circumstances indicate that the three individuals died at the same time, the close range of their ages at death suggests that the individuals were not only genetically related, but that they may have been siblings.

DNA analysis by PCR (polymerase chain reaction), an established tool in forensic paternity testing, has lately been successfully applied to skeletal material (Saiki, 1989; Hagelberg et al., 1989; Herrmann and Hummel, 1994). The introduction of this method to palaeanthropology opens a whole new field of research and will, before long, help to verify many cases of suggested kinship in burials of all epochs. Corroboration of the findings of the odontologic kinship analysis by means of DNA testing is projected for the near future. With regard to the Dolní Věstonice triple burial, the exceptional state of preservation of the individuals as well as the extensive rituals that apparently accompanied their burial are themselves valuable sources of information for the reconstruction of the life and beliefs of ice-age peoples. The results of this investigation will enable us to evaluate hypotheses of biological and social structures of palaeolithic communities by hard scientific evidence and come to sound conclusions in the future.

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